

SEQUENCE LISTING

<110> Kindsvoel, Wayne R.
Topouzis, Stavros

<120> SOLUBLE ZCYTOR11 CYTOKINE RECEPTORS

<130> 00-56

<150> US 60/223,827

<151> 2000-08-08

<150> US 60/250,876

<151> 2000-12-01

<160> 35

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2831

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (34)...(1755)

<400> 1

tagaggccaa gggagggctc tgtgccagcc ccg atg agg acg ctg ctg acc atc	54
Met Arg Thr Leu Leu Thr Ile	
1 5	
ttg act gtg gga tcc ctg gct gct cac gcc cct gag gac ccc tcg gat	102
Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp	
10 15 20	
ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg	150
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu	
25 30 35	
acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc	198

Thr 40	Trp	Asp	Ser	Gly	Pro 45	Glu	Gly	Thr	Pro	Asp 50	Thr	Val	Tyr	Ser	Ile 55	
gag Glu	tat Tyr	aag Lys	acg Thr	tac Tyr	gga Gly	gag Glu	agg Arg	gac Asp	tgg Trp	gtg Val	gca Ala	aag Lys	aag Lys	ggc Gly	tgt Cys	246
				60					65						70	
cag Gln	cgg Arg	atc Ile	acc Thr	cgg Arg	aag Lys	tcc Ser	tgc Cys	aac Asn	ctg Leu	acg Thr	gtg Val	gag Glu	acg Thr	ggc Gly	aac Asn	294
			75					80					85			
ctc Leu	acg Thr	gag Glu	ctc Leu	tac Tyr	tat Tyr	gcc Ala	agg Arg	gtc Val	acc Thr	gct Ala	gtc Val	agt Ser	gcg Ala	gga Gly	ggc Gly	342
		90					95					100				
cgg Arg	tca Ser	gcc Ala	acc Thr	aag Lys	atg Met	act Thr	gac Asp	agg Arg	ttc Phe	agc Ser	tct Ser	ctg Leu	cag Gln	cac His	act Thr	390
	105					110					115					
acc Thr	ctc Leu	aag Lys	cca Pro	cct Pro	gat Asp	gtg Val	acc Thr	tgt Cys	atc Ile	tcc Ser	aaa Lys	gtg Val	aga Arg	tcg Ser	att Ile	438
	120				125					130					135	
cag Gln	atg Met	att Ile	gtt Val	cat His	cct Pro	acc Thr	ccc Pro	acg Thr	cca Pro	atc Ile	cgt Arg	gca Ala	ggc Gly	gat Asp	ggc Gly	486
				140				145						150		
cac His	cgg Arg	cta Leu	acc Thr	ctg Leu	gaa Glu	gac Asp	atc Ile	ttc Phe	cat His	gac Asp	ctg Leu	ttc Phe	tac Tyr	cac His	tta Leu	534
			155					160					165			
gag Glu	ctc Leu	cag Gln	gtc Val	aac Asn	cgc Arg	acc Thr	tac Tyr	caa Gln	atg Met	cac His	ctt Leu	gga Gly	ggg Gly	aag Lys	cag Gln	582
		170					175					180				
aga Arg	gaa Glu	tat Tyr	gag Glu	ttc Phe	ttc Phe	ggc Gly	ctg Leu	acc Thr	cct Pro	gac Asp	aca Thr	gag Glu	ttc Phe	ctt Leu	ggc Gly	630
	185					190					195					
acc Thr	atc Ile	atg Met	att Ile	tgc Cys	gtt Val	ccc Pro	acc Thr	tgg Trp	gcc Ala	aag Lys	gag Glu	agt Ser	gcc Ala	ccc Pro	tac Tyr	678
	200				205					210					215	

ttc tac gcc cca cag gcc atc tct aag gtc cag cct tcc tcc tat gcc 1206
Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala
380 385 390

cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg 1254
 Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met
 395 400 405

gaa ggt tct ggc aaa gac tcc ccc act ggg aca ctt tct agt cct aaa 1302
 Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys
 410 415 420

cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc 1350
 His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser
 425 430 435

tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg 1398
 Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met
 440 445 450 455

gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc 1446
 Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys
 460 465 470

aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg 1494
 Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly
 475 480 485

aca cca cag tac cta aag ggc cag ctc ccc ctc ctc tcc tca gtc cag 1542
 Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln
 490 495 500

atc gag ggc cac ccc atg tcc ctc cct ttg caa cct cct tcc ggt cca 1590
 Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro
 505 510 515

tgt tcc ccc tcg gac caa ggt cca agt ccc tgg ggc ctg ctg gag tcc 1638
 Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser
 520 525 530 535

ctt gtg tgt ccc aag gat gaa gcc aag agc cca gcc cct gag acc tca 1686
 Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser
 540 545 550

gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc 1734

1254 1302 1350 1398 1446 1494 1542 1590 1638 1686 1734

Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala
 555 560 565

ctg act gtg cag tgg gag tcc tgaggggaat gggaaaggct tgggtgcttcc 1785
 Leu Thr Val Gln Trp Glu Ser
 570

tccctgtccc taccagtggt cacatccttg gctgtcaatc ccatgcctgc ccatgccaca 1845
 cactctgcga tctggcctca gacgggtgcc cttgagagaa gcagaggag tggcatgcag 1905
 ggcccctgcc atgggtgctc tcctcaccgg aacaaagcag catgataagg actgcagcgg 1965
 gggagctctg gggagcagct tgtgtagaca agcgcgtgct cgctgagccc tgcaaggcag 2025
 aaatgacagt gcaaggagga aatgcaggga aactcccag gtccagagcc ccacctccta 2085
 acaccatgga ttcaaagtgc tcagggaatt tgccctctct tgccccattc ctggccagtt 2145
 tcacaatcta gctcgacaga gcatgaggcc cctgcctctt ctgtcattgt tcaaagggtg 2205
 gaagagagcc tggaaaagaa ccaggcctgg aaaagaacca gaaggaggct gggcagaacc 2265
 agaacaacct gcacttctgc caaggccagg gccagcagga cggcaggact ctaggaggagg 2325
 gtgtggcctg cagctcattc ccaggcaggg caactgcctg acgttgcacg atttcagctt 2385
 cattcctctg atagaacaaa gcgaaatgca ggtccaccag ggaggagac acacaagcct 2445
 tttctgcagg caggagtttc agaccctatc ctgagaatgg ggtttgaaag gaagggtgagg 2505
 gctgtggccc ctggacgggt acaataacac actgtactga tgtcacaact ttgcaagctc 2565
 tgccttgggt tcagcccatc tgggctcaaa ttccagcctc accactcaca agctgtgtga 2625
 cttcaaacaa atgaaatcag tgcccagaac ctcggtttcc tcactgtgtg tgtggggatc 2685
 ataacaccta cctcatggag ttgtggtgaa gatgaaatga agtcatgtct ttaaagtgtc 2745
 taatagtgcc tgggtacatg gcagtgccca ataaacggta gctattttaa aaaaaaaaaa 2805
 aaaaaaaaaa atagcggccg cctcga 2831

<210> 2

<211> 574

<212> PRT

<213> Homo sapien

<400> 2

Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
 1 5 10 15
 Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
 20 25 30
 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
 35 40 45
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 50 55 60
 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
 65 70 75 80

Leu	Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	
				85					90					95		
Thr	Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	
			100					105					110			
Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	
		115					120					125				
Ile	Ser	Lys	Val	Arg	Ser	Ile	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	
	130					135					140					
Pro	Ile	Arg	Ala	Gly	Asp	Gly	His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	
145				150						155					160	
His	Asp	Leu	Phe	Tyr	His	Leu	Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln	
			165						170					175		
Met	His	Leu	Gly	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr	
		180						185					190			
Pro	Asp	Thr	Glu	Phe	Leu	Gly	Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp	
		195					200					205				
Ala	Lys	Glu	Ser	Ala	Pro	Tyr	Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp	
	210					215					220					
Arg	Thr	Trp	Thr	Tyr	Ser	Phe	Ser	Gly	Ala	Phe	Leu	Phe	Ser	Met	Gly	
225				230						235					240	
Phe	Leu	Val	Ala	Val	Leu	Cys	Tyr	Leu	Ser	Tyr	Arg	Tyr	Val	Thr	Lys	
			245						250					255		
Pro	Pro	Ala	Pro	Pro	Asn	Ser	Leu	Asn	Val	Gln	Arg	Val	Leu	Thr	Phe	
		260						265					270			
Gln	Pro	Leu	Arg	Phe	Ile	Gln	Glu	His	Val	Leu	Ile	Pro	Val	Phe	Asp	
	275						280					285				
Leu	Ser	Gly	Pro	Ser	Ser	Leu	Ala	Gln	Pro	Val	Gln	Tyr	Ser	Gln	Ile	
	290					295					300					
Arg	Val	Ser	Gly	Pro	Arg	Glu	Pro	Ala	Gly	Ala	Pro	Gln	Arg	His	Ser	
305				310						315					320	
Leu	Ser	Glu	Ile	Thr	Tyr	Leu	Gly	Gln	Pro	Asp	Ile	Ser	Ile	Leu	Gln	
			325						330					335		
Pro	Ser	Asn	Val	Pro	Pro	Pro	Gln	Ile	Leu	Ser	Pro	Leu	Ser	Tyr	Ala	
		340						345					350			
Pro	Asn	Ala	Ala	Pro	Glu	Val	Gly	Pro	Pro	Ser	Tyr	Ala	Pro	Gln	Val	
		355					360					365				
Thr	Pro	Glu	Ala	Gln	Phe	Pro	Phe	Tyr	Ala	Pro	Gln	Ala	Ile	Ser	Lys	
	370					375					380					
Val	Gln	Pro	Ser	Ser	Tyr	Ala	Pro	Gln	Ala	Thr	Pro	Asp	Ser	Trp	Pro	
385				390						395					400	
Pro	Ser	Tyr	Gly	Val	Cys	Met	Glu	Gly	Ser	Gly	Lys	Asp	Ser	Pro	Thr	
			405						410					415		

Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln
 420 425 430
 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
 435 440 445
 Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
 450 455 460
 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
 465 470 475 480
 Leu His Ser Gly Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
 485 490 495
 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
 500 505 510
 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
 515 520 525
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
 530 535 540
 Ser Pro Ala Pro Glu Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp
 545 550 555 560
 Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser
 565 570

<210> 3
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 3

Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser Ser
 1 5 10 15
 Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro
 20 25 30
 Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
 35 40 45
 Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
 50 55 60
 Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
 65 70 75 80
 Ala Val Ser Ala Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
 85 90 95
 Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile
 100 105 110

<210> 4
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Glu-Glu peptide tag

<210> 5
<211> 8
<212> PRT
<213> Artificial Sequence

<400> 5
 Tyr Lys Asp Asp Asp Asp Lys
 5

<210>	6
<211>	699
<212>	DNA

<213> Homo sapiens

<400> 6

gagcccagat	cttcagacaa	aactcacaca	tgcccaccgt	gcccagcacc	tgaagccgag	60
ggggcaccgt	cagtcttct	cttccccca	aaacccaagg	acaccctcat	gatctcccgg	120
acccctgagg	tcacatgctg	ggtggtggac	gtgagccacg	aagaccctga	ggtcaagttc	180
aactggtacg	tggacggcgt	ggaggtgcat	aatgccaaga	caaagccgcg	ggaggagcag	240
tacaacagca	cgtaccgtgt	ggtcagcgtc	ctcaccgtcc	tgcaccagga	ctggctgaat	300
ggcaaggagt	acaagtgcaa	ggtctccaac	aaagccctcc	catcctccat	cgagaaaacc	360
atctccaaag	ccaaagggca	gccccgagaa	ccacaggtgt	acaccctgcc	cccatcccgg	420
gatgagctga	ccaagaacca	ggtcagcctg	acctgcctgg	tcaaaggctt	ctatcccagc	480
gacatcgccg	tggagtggga	gagcaatggg	cagccggaga	acaactacaa	gaccacgcct	540
cccgtgctgg	actccgacgg	ctcttcttc	ctctacagca	agctcaccgt	ggacaagagc	600
aggtggcagc	aggggaacgt	cttctcatgc	tccgtgatgc	atgaggctct	gcacaaccac	660
tacacgcaga	agagcctctc	cctgtctccg	ggtaaataa			699

<210> 7

<211> 1116

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (21)...(557)

<400> 7

tcgagttaga	attgtctgca	atg gcc gcc	ctg cag aaa	tct gtg agc	tct ttc	53
		Met Ala Ala	Leu Gln Lys	Ser Val Ser	Ser Phe	
		1	5	10		
ctt atg ggg	acc ctg gcc	acc agc tgc	ctc ctt ctc	ttg gcc ctc	ttg	101
Leu Met Gly	Thr Leu Ala	Thr Ser Cys	Leu Leu Leu	Leu Ala Leu	Leu	
	15	20	25			
gta cag gga	gga gca gct	gcg ccc atc	agc tcc cac	tgc agg ctt	gac	149
Val Gln Gly	Gly Ala Ala	Ala Pro Ile	Ser Ser His	Cys Arg Leu	Asp	
	30	35	40			
aag tcc aac	ttc cag cag	ccc tat atc	acc aac cgc	acc ttc atg	ctg	197
Lys Ser Asn	Phe Gln Gln	Pro Tyr Ile	Thr Asn Arg	Thr Phe Met	Leu	
	45	50	55			
gct aag gag	gct agc ttg	gct gat aac	aac aca gac	gtt cgt ctc	att	245

T00000-55092660

Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile
 60 65 70 75
 ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg 293
 Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu
 80 85 90
 atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa 341
 Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln
 95 100 105
 tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc 389
 Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala
 110 115 120
 agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg 437
 Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu
 125 130 135
 cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485
 His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu
 140 145 150 155
 gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533
 Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe
 160 165 170
 atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac 587
 Met Ser Leu Arg Asn Ala Cys Ile
 175
 taaccccctt tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca 647
 aaaggaagat gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt 707
 tagttacaaa ggaaaccaat gccacttttg tttataagac cagaaggtag actttctaag 767
 catagatatt tattgataac atttcattgt aactggtggt ctatacacag aaaacaattt 827
 attttttaaa taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa 887
 aaacccttaa atagcttcat gtttcataaa tcagtacttt atatttataa atgtatttat 947
 tattattata agactgcatt ttatttatat cattttatta atatggattt atttatagaa 1007
 acatcattcg atattgctac ttgagtgtaa ggctaataatt gatatttatg acaataatta 1067
 tagagctata acatgtttat ttgacctcaa taaacacttg gatataccta 1116

<210> 8

<211> 179

<212> PRT

<213> homo sapiens

<400> 8

Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu
 1 5 10 15
 Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala
 20 25 30
 Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
 35 40 45
 Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
 50 55 60
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
 65 70 75 80
 His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
 85 90 95
 Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
 100 105 110
 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
 115 120 125
 Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
 130 135 140
 Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
 145 150 155 160
 Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
 165 170 175
 Ala Cys Ile

<210> 9

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide prime ZC28590

<400> 9

ttgggtacct ctgcaatggc cgccctgcag aaatct

36

<210> 10

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide prime ZC28580

<400> 10

ttgggatcca atgcaggcat ttctcagaga cat

33

<210> 11

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide prime ZC14666

<400> 11

agccaccaag atgactga

18

<210> 12

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide prime ZC14742

<400> 12

tgcatttggt aggtgcggtt ga

22

<210> 13

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> His tag

<400> 13

His His His His His His

1

5

<210> 14

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29239

<400> 14

gaggccgcat	ccggttcggg	ttcgggttcg	gagcccagat	catcagacaa	aactcacaca	60
tgc						63

<210> 15

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29232

<400> 15

cgactgactc	gagtcagtga	tggtgatggt	gatggccacc	tgatccttta	cccggagaca	60
gggag						65

<210> 16

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39319

<400> 16

atcggaattc	gcagaagcca	tggcgtggag	ccttggg	37
------------	------------	------------	---------	----

<210> 17

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39325

<400> 17

cagtggatcc	ggaggggacc	gtttcgtc	28
------------	------------	----------	----

```
<220>  
<221> CDS  
<222> (1)...(660)
```

atg gcg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca 48
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
1 5 10 15

gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt 96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
20 25 30

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg 144
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
35 40 45

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat 192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
50 55 60

aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc 240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65 70 75 80

aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag 288
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
85 90 95

cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att 336
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
100 105 110

att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat 384
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
115 120 125

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act 432
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa 480
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160

aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag 528
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175

gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga 576
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190

ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc 624
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205

tgt gag caa aca acc cat gac gaa acg gtc ccc tcc 660
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
 210 215 220

<210> 19

<211> 220

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
 1 5 10 15
 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
 20 25 30
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
 35 40 45
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
 50 55 60
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
 65 70 75 80
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
 85 90 95

His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
 100 105 110
 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
 115 120 125
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
 130 135 140
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
 145 150 155 160
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
 165 170 175
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
 180 185 190
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
 195 200 205
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
 210 215 220

<210> 20

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC38931

<400> 20

acaaagccgc gggaggag

18

<210> 21

<211> 82

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC39042

<400> 21

ctgactcgag tcagtgatgg tgatggtgat ggccacctga tccggaacca cgcggaacca
 gtttaccgag agacaggag ag

60

82

<210> 22

<211> 1428

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(1428)

<223> CRF2-4 extracellular cytokine binding domain fused
to IgGg1 with a 6-HIS tag

<400> 22

atg	gcg	tgg	agt	ctt	ggg	agc	tgg	ctg	ggt	ggc	tgc	ctg	ctg	gtg	tca	48
Met	Ala	Trp	Ser	Leu	Gly	Ser	Trp	Leu	Gly	Gly	Cys	Leu	Leu	Val	Ser	
1				5				10						15		

gca	ttg	gga	atg	gta	cca	cct	ccc	gaa	aat	gtc	aga	atg	aat	tct	gtt	96
Ala	Leu	Gly	Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val	
			20					25						30		

aat	ttc	aag	aac	att	cta	cag	tgg	gag	tca	cct	gct	ttt	gcc	aaa	ggg	144
Asn	Phe	Lys	Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	
		35					40					45				

aac	ctg	act	ttc	aca	gct	cag	tac	cta	agt	tat	agg	ata	ttc	caa	gat	192
Asn	Leu	Thr	Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	
	50					55					60					

aaa	tgc	atg	aat	act	acc	ttg	acg	gaa	tgt	gat	ttc	tca	agt	ctt	tcc	240
Lys	Cys	Met	Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	
65					70				75					80		

aag	tat	ggt	gac	cac	acc	ttg	aga	gtc	agg	gct	gaa	ttt	gca	gat	gag	288
Lys	Tyr	Gly	Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	
				85				90						95		

cat	tca	gac	tgg	gta	aac	atc	acc	ttc	tgt	cct	gtg	gat	gac	acc	att	336
His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	
			100					105					110			

att	gga	ccc	cct	gga	atg	caa	gta	gaa	gta	ctt	gat	gat	tct	tta	cat	384
Ile	Gly	Pro	Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Asp	Asp	Ser	Leu	His	
		115					120					125				

atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act	432
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr	
130 135 140	
atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa	480
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys	
145 150 155 160	
aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag	528
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu	
165 170 175	
gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga	576
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg	
180 185 190	
ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc	624
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val	
195 200 205	
tgt gag caa aca acc cat gac gaa acg gtc ccc tcc gga tcc ggt tcg	672
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser	
210 215 220	
ggt tcg ggt tcg gag ccc aga tca tca gac aaa act cac aca tgc cca	720
Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro	
225 230 235 240	
ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc	768
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe	
245 250 255	
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc	816
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	
260 265 270	
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc	864
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	
275 280 285	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg	912
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	
290 295 300	

cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	960
Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	
305					310					315					320	
gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	1008
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	
				325					330					335		
tcc	aac	aaa	gcc	ctc	cca	tcc	tcc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	1056
Ser	Asn	Lys	Ala	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	
			340					345					350			
aaa	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	1104
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	
		355					360					365				
gat	gag	ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	1152
Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	
	370					375					380					
ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	1200
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	
385					390					395					400	
gag	aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	1248
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	
				405					410					415		
ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	1296
Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	
			420					425					430			
ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	1344
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	
		435					440					445				
tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggt	aaa	ctg	gtt	ccg	cgt	1392
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Leu	Val	Pro	Arg	
	450					455					460					
ggt	tcc	gga	tca	ggt	ggc	cat	cac	cat	cac	cat	cac					1428

```
<210> 23
<211> 476
<212> PRT
<213> Homo sapiens
```

<400> 23															
Met	Ala	Trp	Ser	Leu	Gly	Ser	Trp	Leu	Gly	Gly	Cys	Leu	Leu	Val	Ser
1				5				10						15	
Ala	Leu	Gly	Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val
			20					25					30		
Asn	Phe	Lys	Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly
		35				40						45			
Asn	Leu	Thr	Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp
	50					55					60				
Lys	Cys	Met	Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser
65					70					75					80
Lys	Tyr	Gly	Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu
				85					90					95	
His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile
			100					105					110		
Ile	Gly	Pro	Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Asp	Asp	Ser	Leu	His
		115				120						125			
Met	Arg	Phe	Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr
	130					135						140			
Met	Lys	Asn	Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys
145					150					155					160
Asn	Gly	Thr	Asp	Glu	Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu
				165				170						175	
Val	Leu	Arg	Asn	Leu	Glu	Pro	Trp	Thr	Thr	Tyr	Cys	Val	Gln	Val	Arg
			180					185					190		
Gly	Phe	Leu	Pro	Asp	Arg	Asn	Lys	Ala	Gly	Glu	Trp	Ser	Glu	Pro	Val
		195					200					205			
Cys	Glu	Gln	Thr	Thr	His	Asp	Glu	Thr	Val	Pro	Ser	Gly	Ser	Gly	Ser
	210					215					220				
Gly	Ser	Gly	Ser	Glu	Pro	Arg	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro
225					230					235					240
Pro	Cys	Pro	Ala	Pro	Glu	Ala	Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe
				245					250					255	

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 260 265 270
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 275 280 285
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 290 295 300
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 305 310 315 320
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 325 330 335
 Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
 340 345 350
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 355 360 365
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 370 375 380
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 385 390 395 400
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 405 410 415
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
 420 425 430
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
 435 440 445
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg
 450 455 460
 Gly Ser Gly Ser Gly Gly His His His His His His
 465 470 475

<210> 24

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC29328

<400> 24

tcagagggat ccggttcggg ttcgggttcg gagcccagat catcagacaa aactcacaca
 tgc

60

63

<210> 25

<213> Artificial Sequence

<223> Oligonucleotide primer ZC29231

cgactgactc gagctactcc ataggcatat actcgccacc tgatccttta cccggagaca 60
gggag 65

<213> Artificial Sequence

<223> Oligonucleotide primer ZC39335

atcggaattc gcagaagcca tgaggacgct gctgaccatc ttgactgtgg ggtccctggc 60
tgctcacgcc 70

<213> Artificial Sequence

<223> Oligonucleotide primer ZC28981

tttgggctcc ctgagctctg gtggaa 26

<213> Artificial Sequence

<223> Oligonucleotide primer ZC39043

<400> 28

<210> 29
<211> 1452
<212> DNA
<213> Artificial Sequence

<220>
<223> hzcytor11 extracellular cytokine binding domain
fused to IgGg1 with a Glu-Glu tag

<221> CDS
<222> (1)...(1452)

<400> 29																	
atg	agg	acg	ctg	ctg	acc	atc	ttg	act	gtg	gga	tcc	ctg	gct	gct	cac	48	
Met	Arg	Thr	Leu	Leu	Thr	Ile	Leu	Thr	Val	Gly	Ser	Leu	Ala	Ala	His		
1			5			10			15								
gcc	cct	gag	gac	ccc	tcg	gat	ctg	ctc	cag	cac	gtg	aaa	ttc	cag	tcc	96	
Ala	Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser		
20				25				30									
agc	aac	ttt	gaa	aac	atc	ctg	acg	tgg	gac	agc	ggg	cca	gag	ggc	acc	144	
Ser	Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr		
35			40			45											
cca	gac	acg	gtc	tac	agc	atc	gag	tat	aag	acg	tac	gga	gag	agg	gac	192	
Pro	Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp		
50		55		60													
tgg	gtg	gca	aag	aag	ggc	tgt	cag	cgg	atc	acc	cgg	aag	tcc	tgc	aac	240	
Trp	Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn		
65		70			75			80									
ctg	acg	gtg	gag	acg	ggc	aac	ctc	acg	gag	ctc	tac	tat	gcc	agg	gtc	288	
Leu	Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val		
85				90				95									
acc	gct	gtc	agt	gcg	gga	ggc	cgg	tca	gcc	acc	aag	atg	act	gac	agg	336	
Thr	Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg		
100			105			110											

ttc agc tct ctg cag cac act acc ctc aag cca cct gat gtg acc tgt	384
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys	
115 120 125	
atc tcc aaa gtg aga tcg att cag atg att gtt cat cct acc ccc acg	432
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr	
130 135 140	
cca atc cgt gca ggc gat ggc cac cgg cta acc ctg gaa gac atc ttc	480
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe	
145 150 155 160	
cat gac ctg ttc tac cac tta gag ctc cag gtc aac cgc acc tac caa	528
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln	
165 170 175	
atg cac ctt gga ggg aag cag aga gaa tat gag ttc ttc ggc ctg acc	576
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr	
180 185 190	
cct gac aca gag ttc ctt ggc acc atc atg att tgc gtt ccc acc tgg	624
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp	
195 200 205	
gcc aag gag agt gcc ccc tac atg tgc cga gtg aag aca ctg cca gac	672
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp	
210 215 220	
cgg aca tgg acc gga tcc ggt tcg ggt tcg ggt tcg gag ccc aga tca	720
Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser	
225 230 235 240	
tca gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag	768
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu	
245 250 255	
ggg gca ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc	816
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	
260 265 270	
atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc	864

Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	
		275					280						285			
cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	912
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	
	290					295					300					
gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	960
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	
305					310					315					320	
tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	1008
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	
				325					330					335		
ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	tcc	tcc	1056
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ser	Ser	
			340					345					350			
atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	cag	1104
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	
		355					360					365				
gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gat	gag	ctg	acc	aag	aac	cag	gtc	1152
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	
	370					375					380					
agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	1200
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	
385					390					395					400	
gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	1248
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	
				405					410					415		
ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	1296
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	
				420				425					430			
gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	1344
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	
		435					440					445				

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg 1392
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460

tct ccg ggt aaa ctg gtt ccg cgt ggt tcc gga tca ggt ggc gag tat 1440
 Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
 465 470 475 480

atg cct atg gag 1452
 Met Pro Met Glu

<210> 30

<211> 484

<212> PRT

<213> Artificial Sequence

<400> 30

Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
 1 5 10 15
 Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
 20 25 30
 Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
 35 40 45
 Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
 50 55 60
 Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
 65 70 75 80
 Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
 85 90 95
 Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
 100 105 110
 Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
 115 120 125
 Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
 130 135 140
 Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
 145 150 155 160
 His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
 165 170 175
 Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
 180 185 190

Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
 195 200 205
 Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
 210 215 220
 Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser
 225 230 235 240
 Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
 245 250 255
 Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 260 265 270
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 290 295 300
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 305 310 315 320
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser
 340 345 350
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 370 375 380
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460
 Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
 465 470 475 480
 Met Pro Met Glu

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<223> Oligonucleotide primer ZC37693

ccccagacac ggtctacagc at

22

<211> 23

<212> DNA

<213> Artificial Sequence

<223> Oligonucleotide primer ZC37449

gggtcaggcc gaagaactca tat

23

<211> 199

<212> PRT

<213> Homo sapiens

Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val	Asn	Phe	Lys
1				5					10					15	
Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	Asn	Leu	Thr
			20					25					30		
Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	Lys	Cys	Met
		35					40					45			
Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	Lys	Tyr	Gly
	50					55					60				
Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	His	Ser	Asp
65				70						75				80	
Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	Ile	Gly	Pro
			85						90					95	
Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Ala	Asp	Ser	Leu	His	Met	Arg	Phe
			100					105					110		
Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	Met	Lys	Asn
		115					120					125			
Val	Tyr	Asn	Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	Asn	Gly	Thr
	130					135					140				

```
<210> 34
<211> 211
<212> PRT
<213> Homo sapiens
```

<400> 34															
Ser	Asp	Ala	His	Gly	Thr	Glu	Leu	Pro	Ser	Pro	Pro	Ser	Val	Trp	Phe
1				5					10					15	
Glu	Ala	Glu	Phe	Phe	His	His	Ile	Leu	His	Trp	Thr	Pro	Ile	Pro	Asn
			20					25					30		
Gln	Ser	Glu	Ser	Thr	Cys	Tyr	Glu	Val	Ala	Leu	Leu	Arg	Tyr	Gly	Ile
		35					40					45			
Glu	Ser	Trp	Asn	Ser	Ile	Ser	Asn	Cys	Ser	Gln	Thr	Leu	Ser	Tyr	Asp
	50					55					60				
Leu	Thr	Ala	Val	Thr	Leu	Asp	Leu	Tyr	His	Ser	Asn	Gly	Tyr	Arg	Ala
65					70					75					80
Arg	Val	Arg	Ala	Val	Asp	Gly	Ser	Arg	His	Ser	Asn	Trp	Thr	Val	Thr
			85					90						95	
Asn	Thr	Arg	Phe	Ser	Val	Asp	Glu	Val	Thr	Leu	Thr	Val	Gly	Ser	Val
			100					105					110		
Asn	Leu	Glu	Ile	His	Asn	Gly	Phe	Ile	Leu	Gly	Lys	Ile	Gln	Leu	Pro
		115					120					125			
Arg	Pro	Lys	Met	Ala	Pro	Ala	Asn	Asp	Thr	Tyr	Glu	Ser	Ile	Phe	Ser
		130				135					140				
His	Phe	Arg	Glu	Tyr	Glu	Ile	Ala	Ile	Arg	Lys	Val	Pro	Gly	Asn	Phe
145					150					155					160
Thr	Phe	Thr	His	Lys	Lys	Val	Lys	His	Glu	Asn	Phe	Ser	Leu	Leu	Thr
				165					170					175	
Ser	Gly	Glu	Val	Gly	Glu	Phe	Cys	Val	Gln	Val	Lys	Pro	Ser	Val	Ala
			180					185				190			
Ser	Arg	Ser	Asn	Lys	Gly	Met	Trp	Ser	Lys	Glu	Glu	Cys	Ile	Ser	Leu
			195				200					205			

```
<210> 35
<211> 201
<212> PRT
<213> Homo sapiens
```

<400> 35															
Asp	Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser
1				5					10					15	
Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro	Gly
			20					25					30		
Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu	Ser	Leu
		35					40					45			
Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser	Leu	Thr	Glu
	50					55					60				
Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala	Thr	Val	Pro	Tyr
65					70					75					80
Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln	Thr	Ser	Ala	Trp	Ser
			85						90					95	
Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	Thr	Ile	Leu	Thr	Arg	Pro
			100					105					110		
Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	His	Leu	Val	Ile	Glu	Leu	Glu
		115					120					125			
Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu
	130					135					140				
Pro	Gly	Ala	Glu	Glu	His	Val	Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro
145					150					155					160
Val	His	Leu	Glu	Thr	Met	Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala
				165					170					175	
Gln	Thr	Phe	Val	Lys	Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr
			180					185					190		
Glu	Cys	Val	Glu	Val	Gln	Gly	Glu	Ala							
		195					200								